

Dialogue between
the microbiota and
the immune system

Yasmine Belkaid



Humans have co-evolved with microbial partners

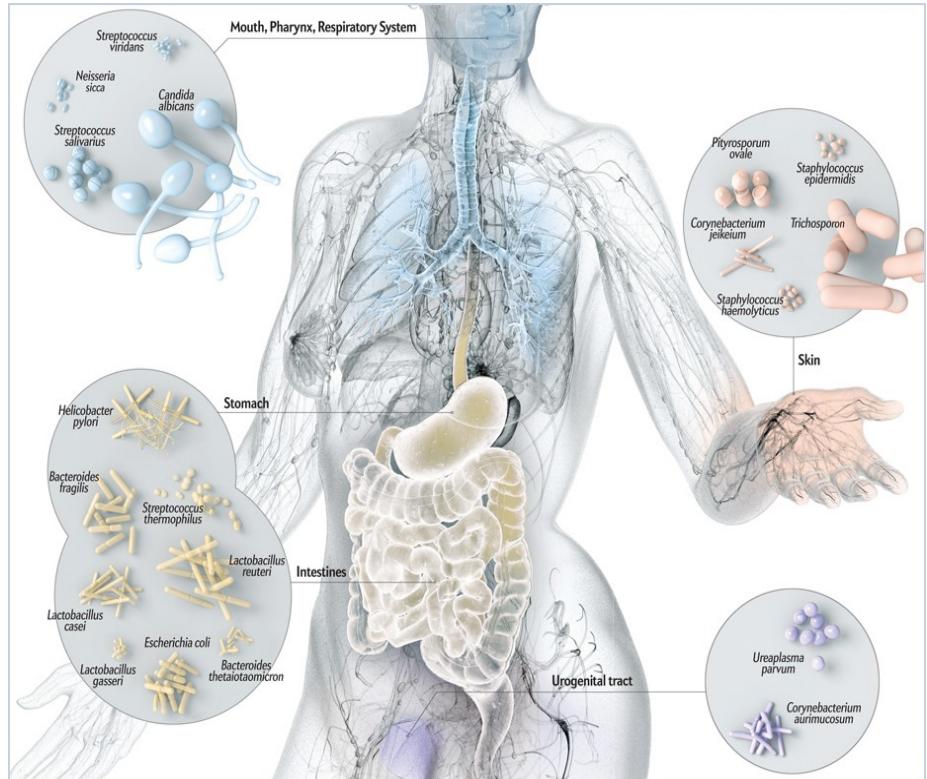


Illustration
Scientific American 2012

- We are a composite of species: bacteria, archaea, protozoan, fungi, viruses, bacteriophages
- Commensal microorganisms
 - inhabit all barrier surfaces of our organism
 - are at least as numerous as human cells
 - their DNA (**the microbiome**) contains 100 times more genes than our 'own' **human genome**
- Humans are metaorganisms composed of host and microbial cells with their own genes and shared metabolic processes and products

Human genome

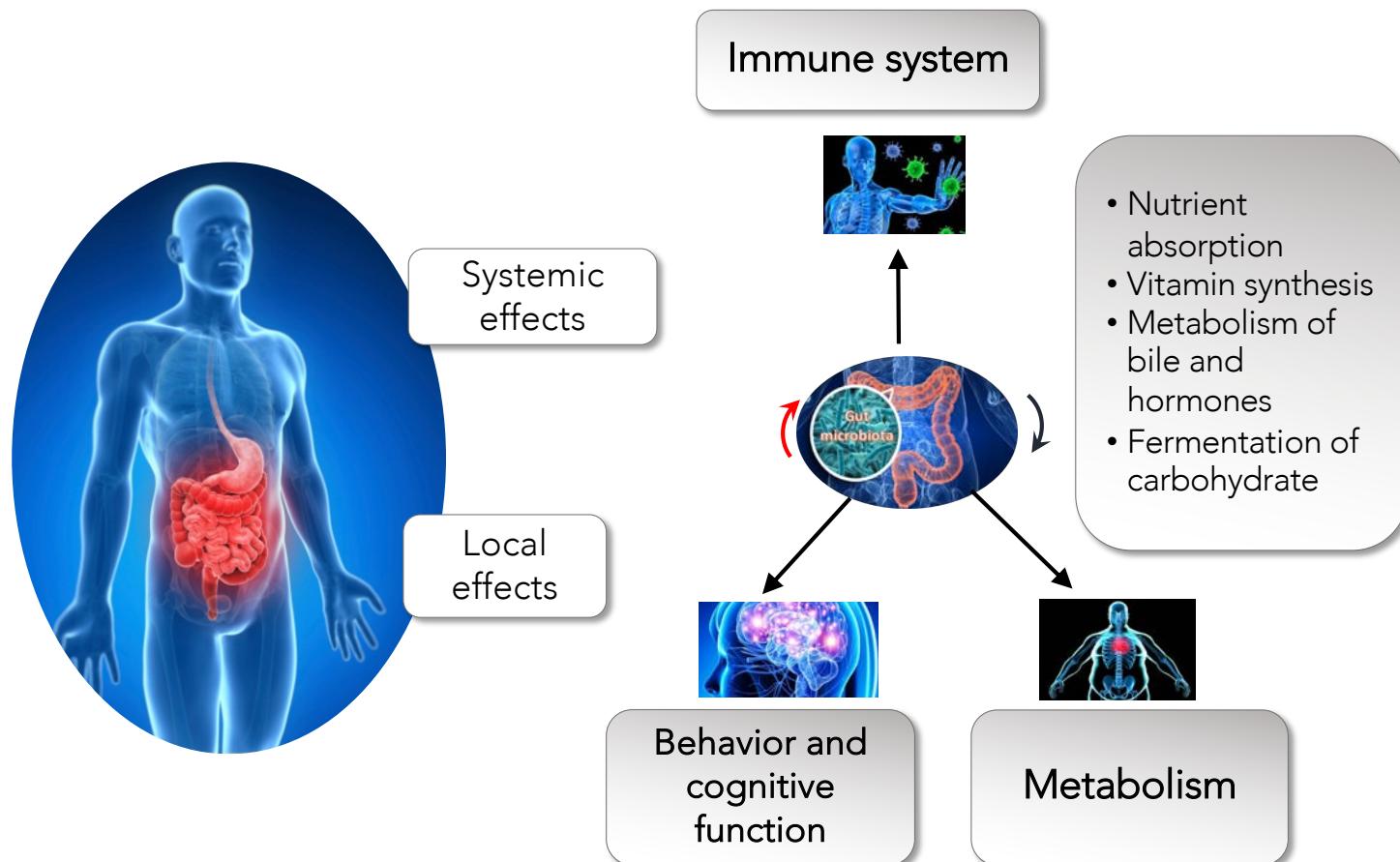


We are a composite of species:
bacterial, fungi, viruses...
a metaorganism

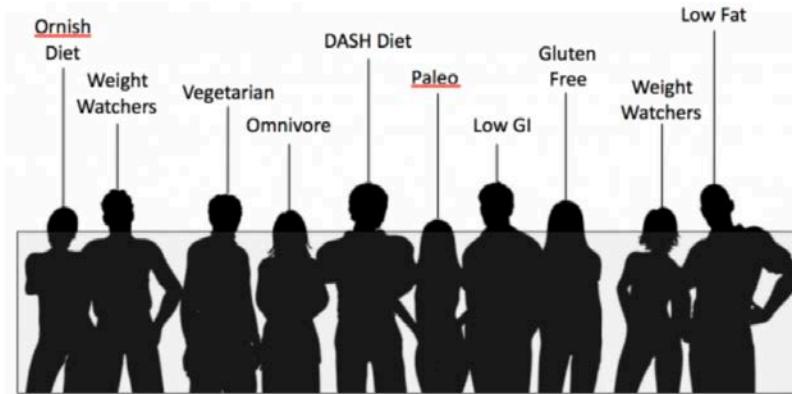
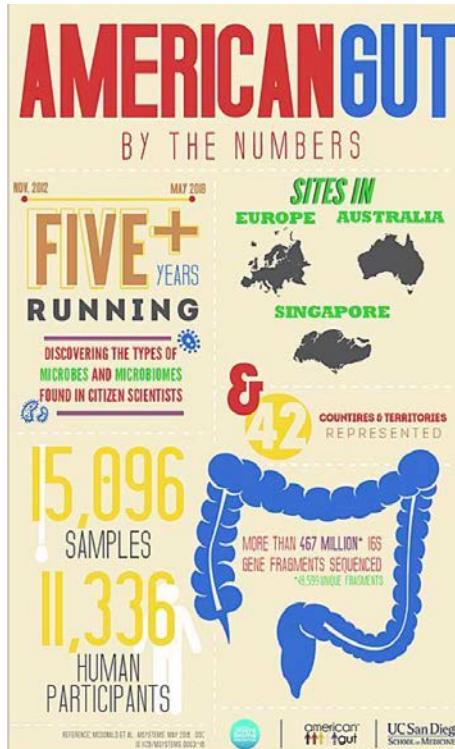


Human microbiome

Control of host physiology by the microbiota



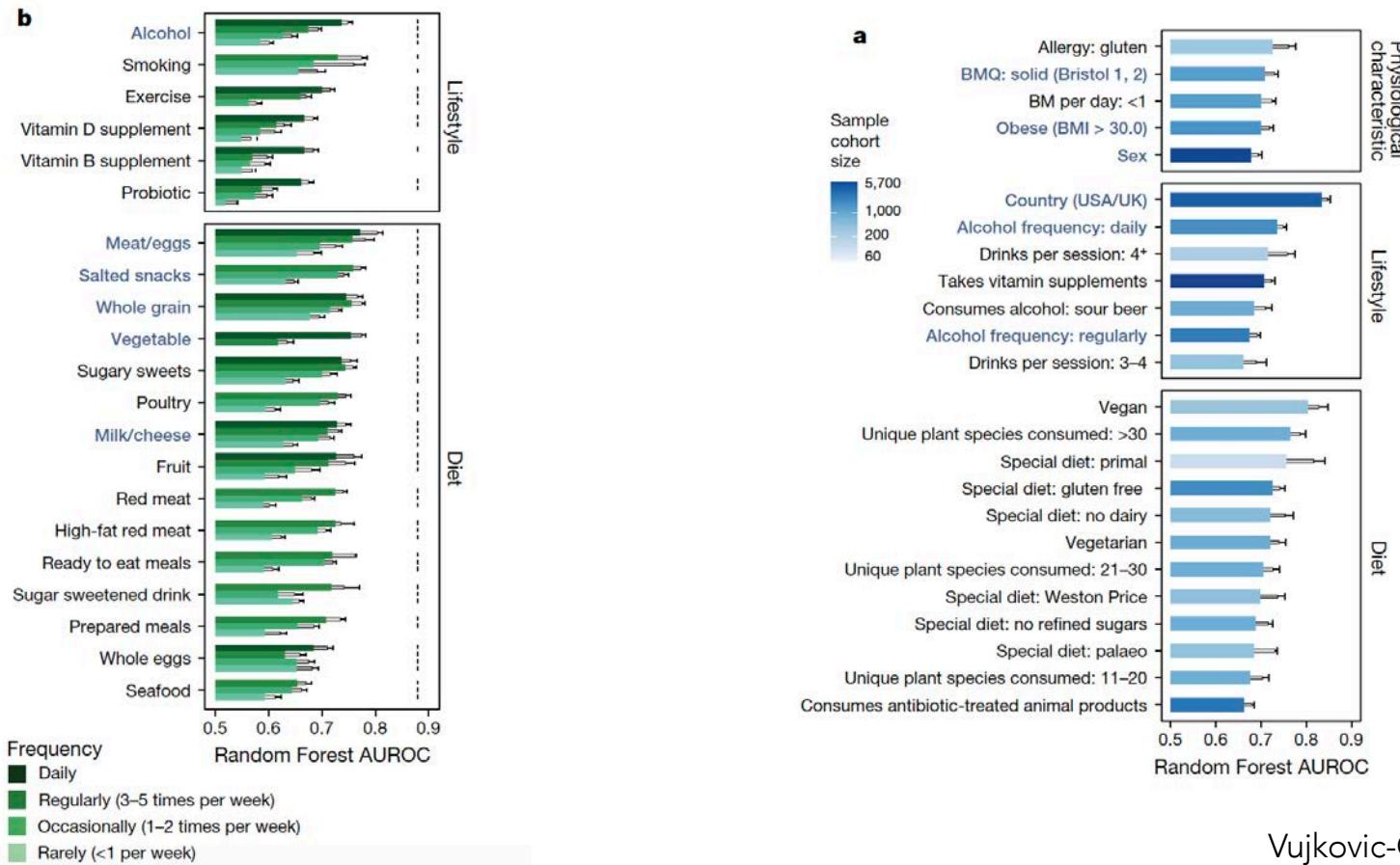
Identifying sources of microbiome heterogeneity across human populations



Ivan Vujkovic-Cvijin

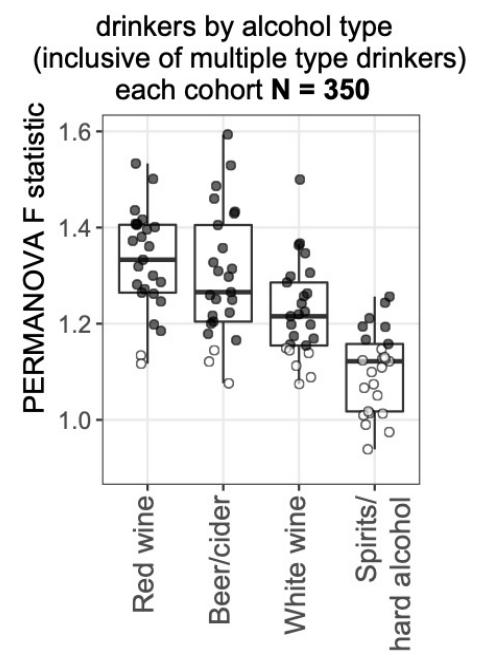
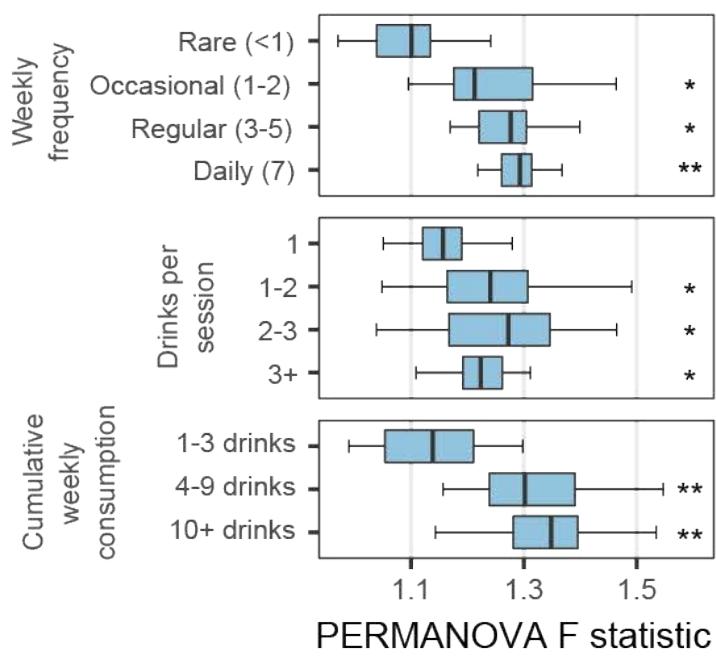
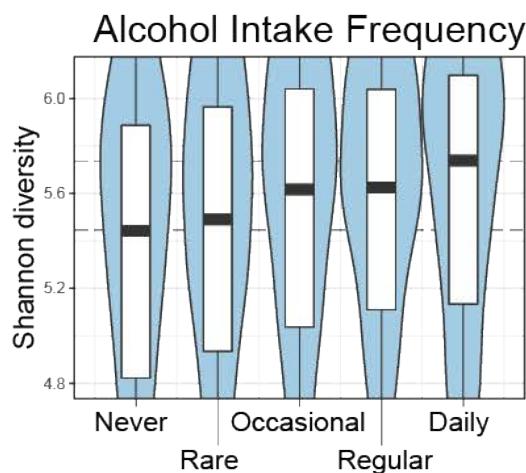


Physiological, lifestyle and dietary characteristics strongly associate with the composition of the gut microbiota



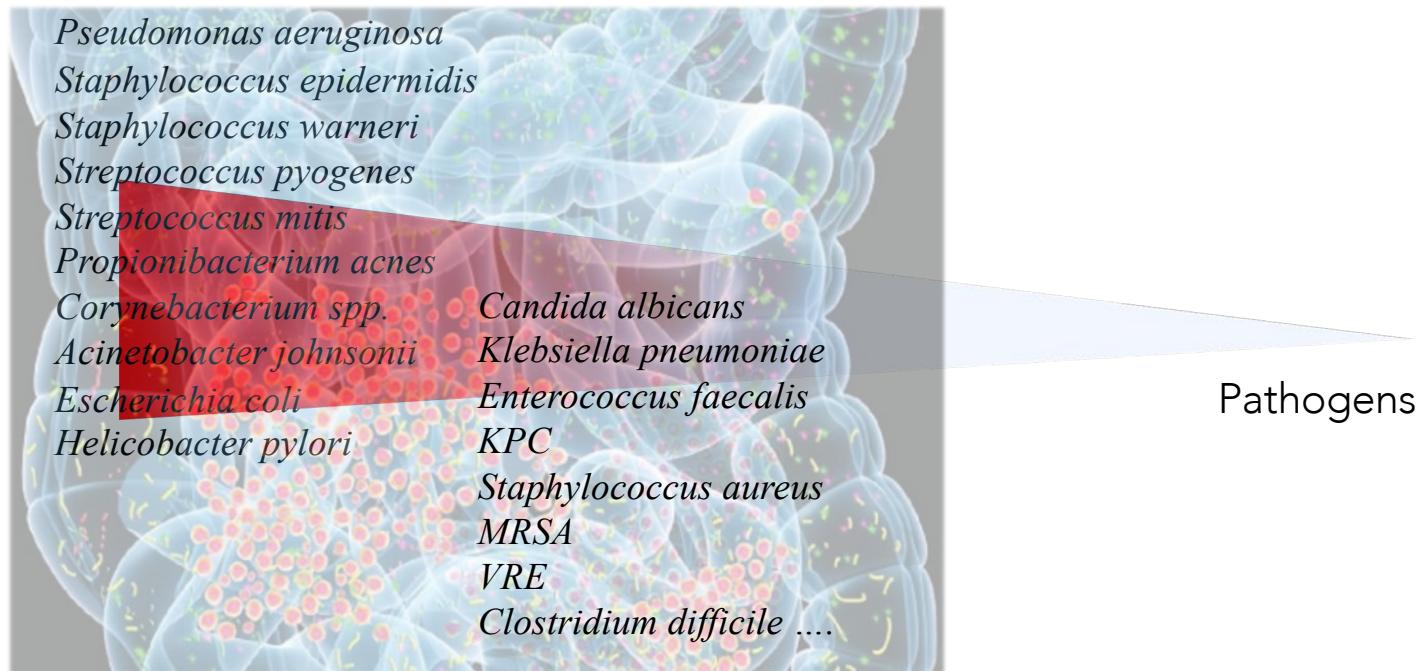
Vujkovic-Cvijin et al, Nature, 2020

Alcohol affects gut microbiota composition in a dose-dependent manner

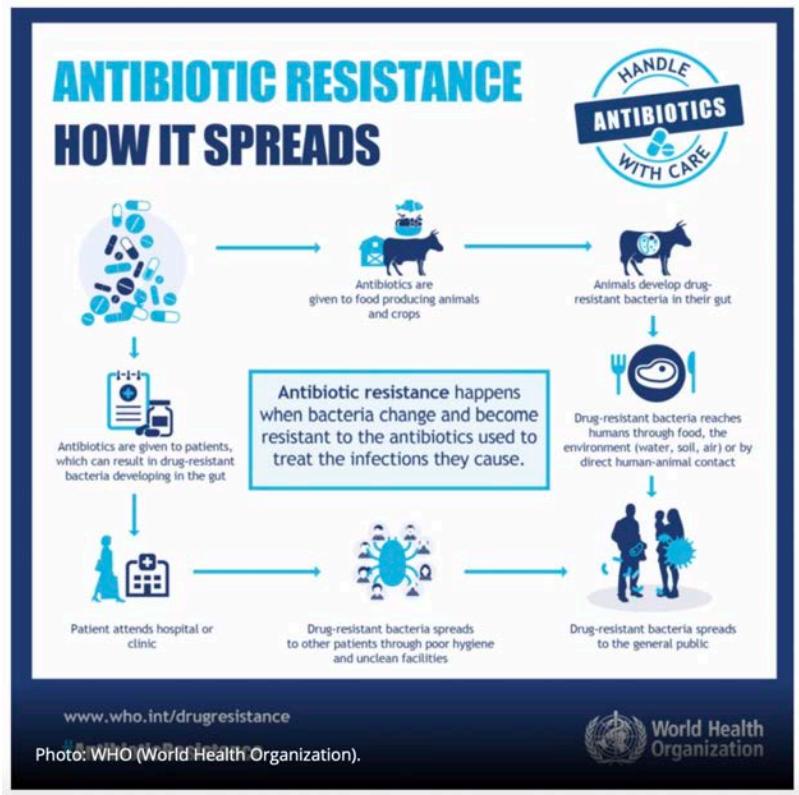


Vujkovic-Cvijin et al, *Nature*, 2020

A large number of microbes able to cause diseases
are normal constituents of the microbiota



Antimicrobial resistance



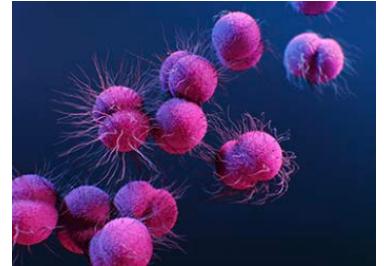
Drug-resistant
Candida auris



Carbapenem-resistant
Enterobacteriaceae (CRE)
Neisseria gonorrhoeae



Drug-resistant
Neisseria gonorrhoeae



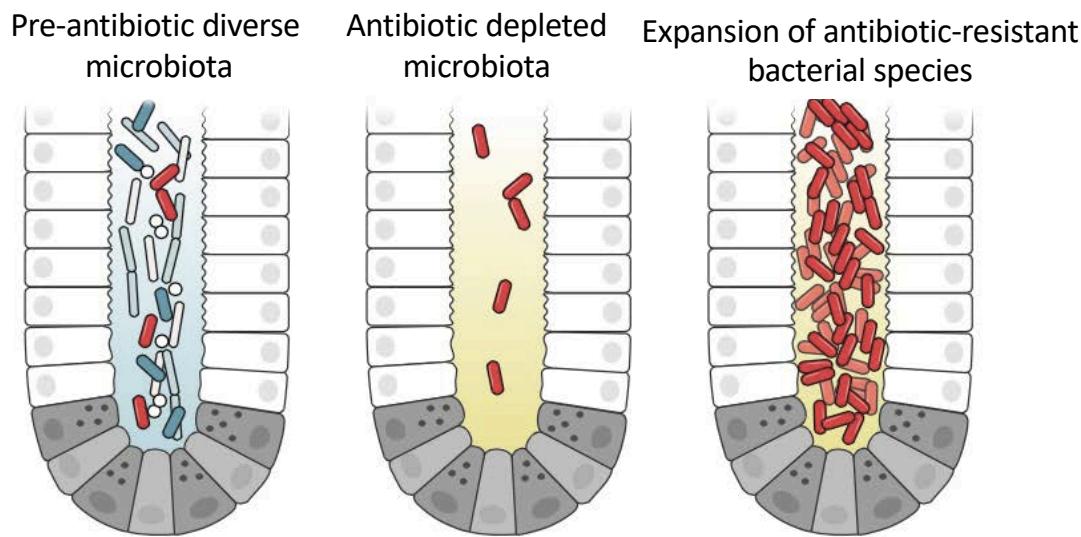
Clostridium difficile



Carbapenem-resistant
Acinetobacter



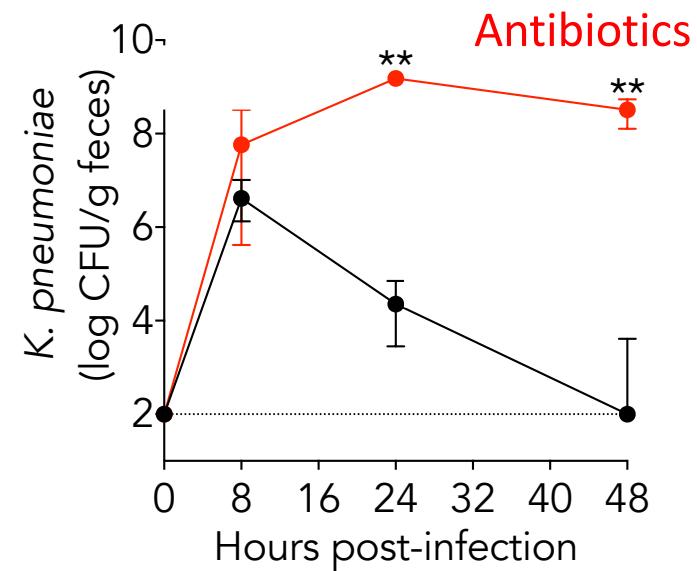
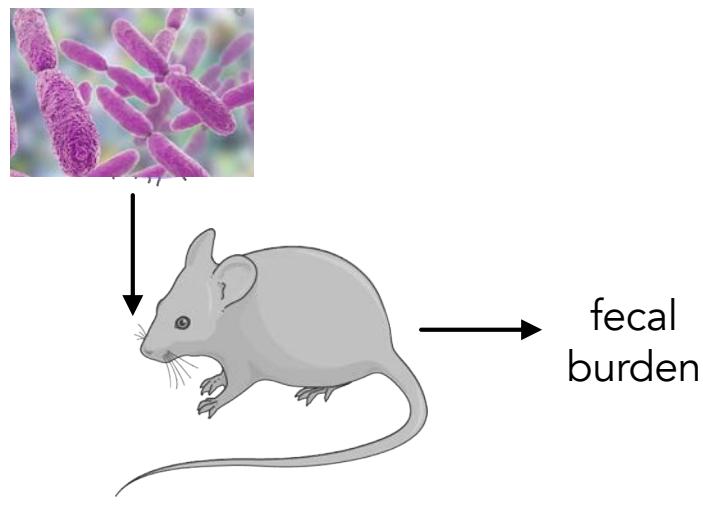
Antibiotic treatment can lead to the expansion of antibiotic resistant species



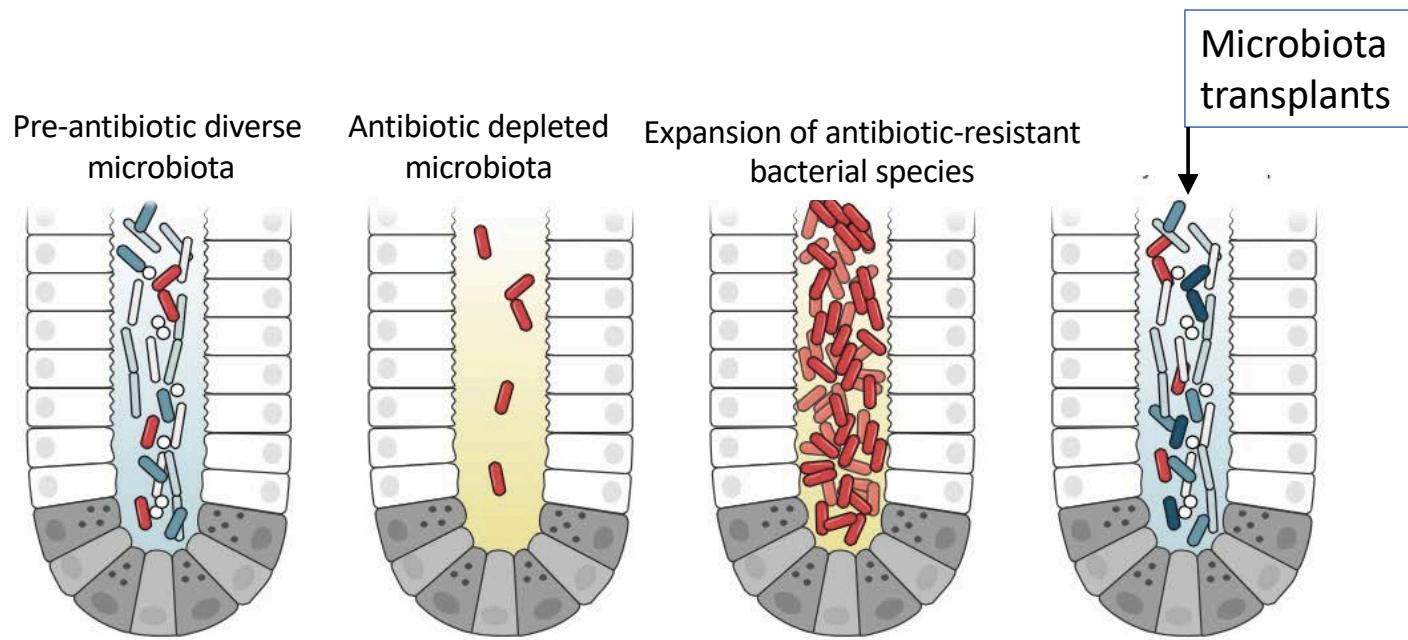
Adapted from Pamer et al, *Science*, 2016

Klebsiella pneumoniae is a major cause of infection in individuals with compromised gut microbiota

Klebsiella pneumoniae

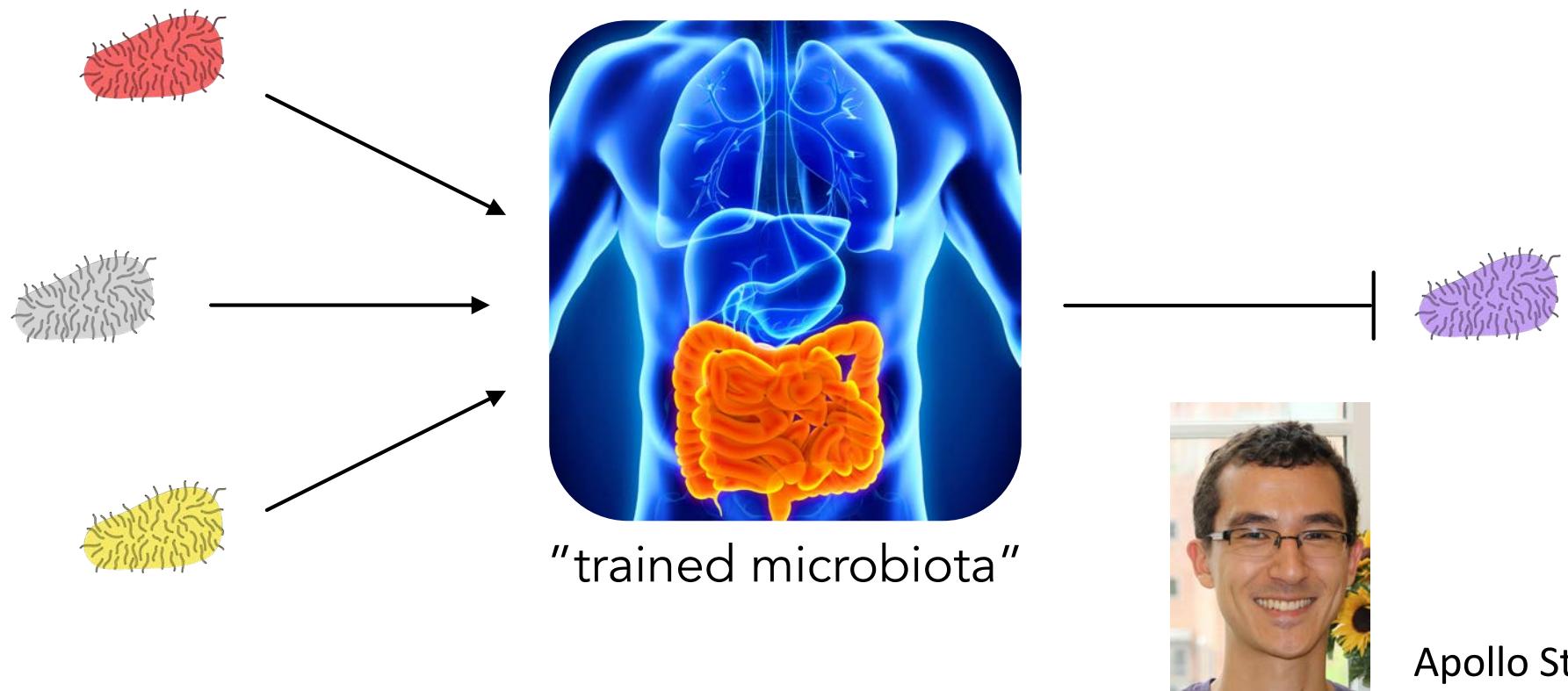


Antibiotic treatment can lead to the expansion of antibiotic resistant species



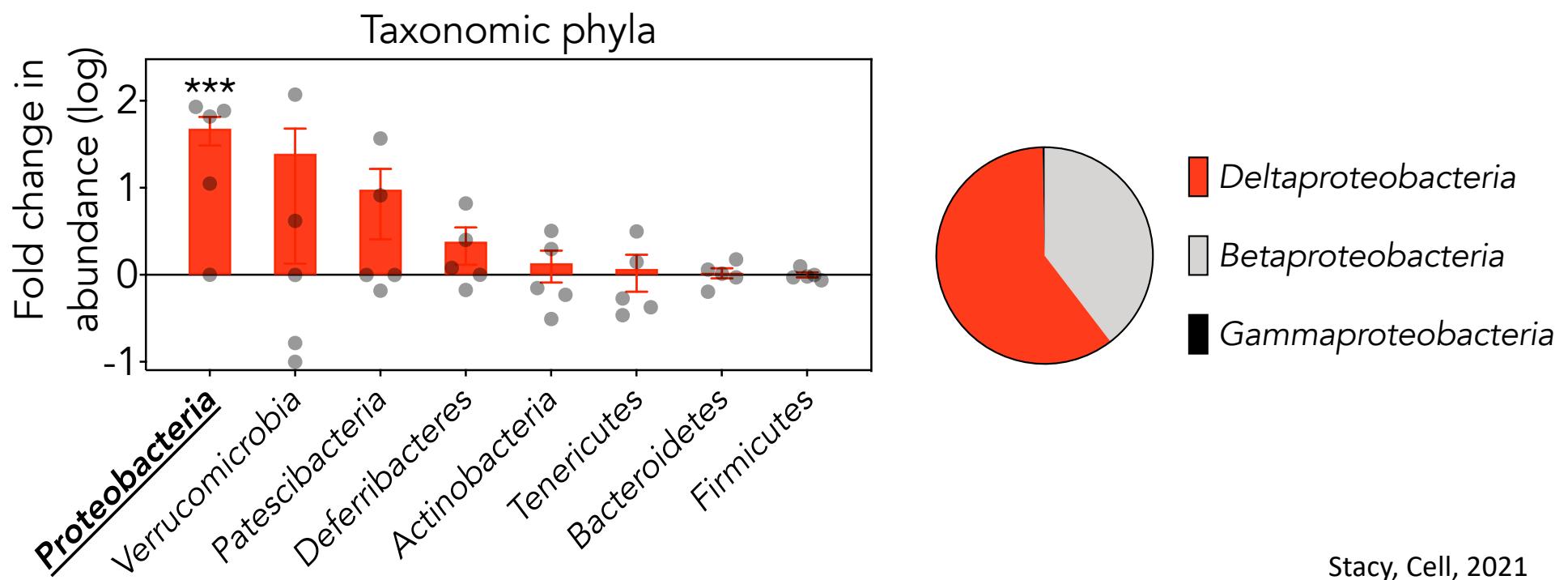
Adapted from Pamer et al, *Science*, 2016

Can pathogen-induced microbiota shield against subsequent infections?

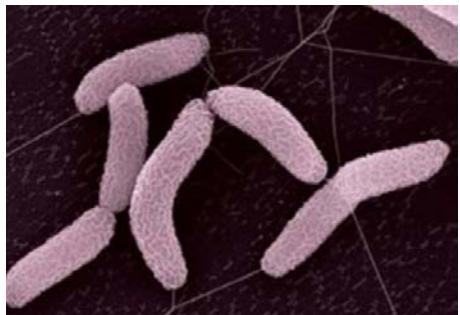


Apollo Stacy

Prior infection elicits an expansion of *Deltaproteobacteria*

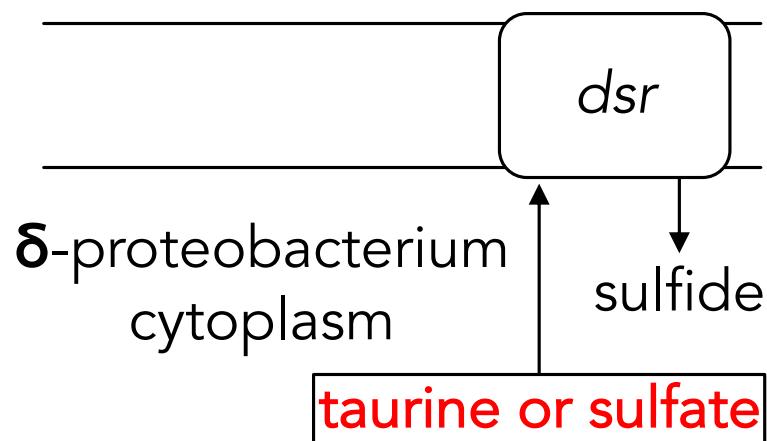


Stacy, Cell, 2021

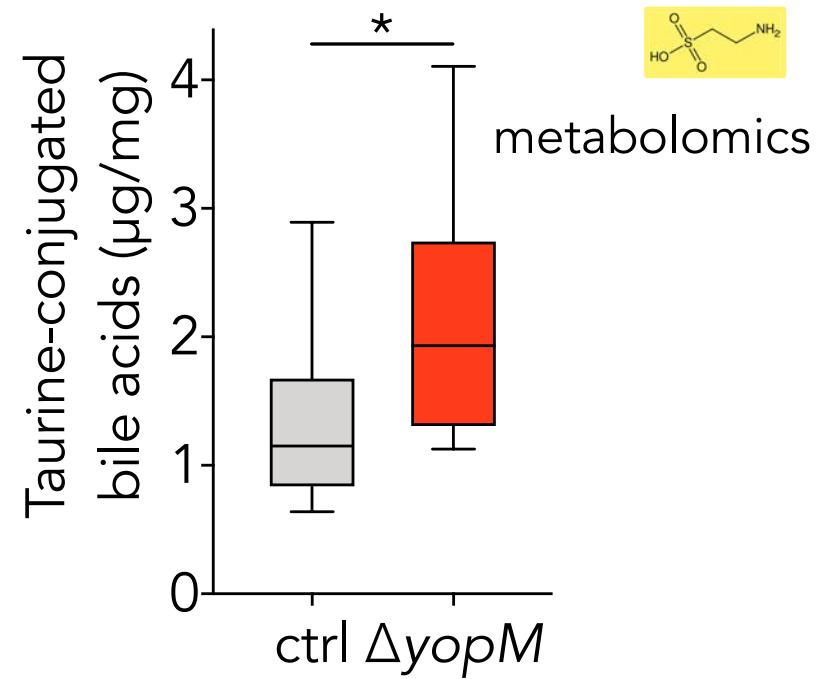
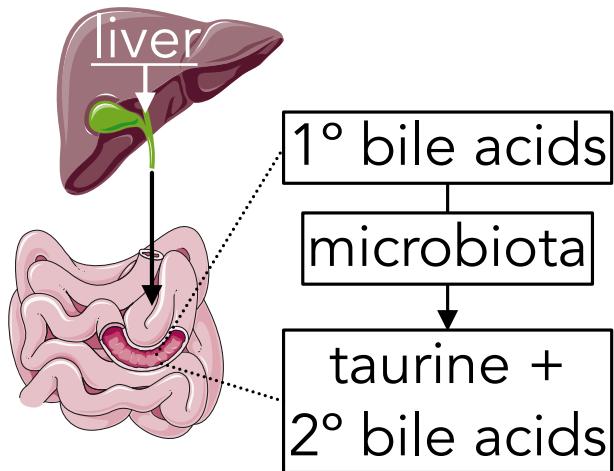


Deltaproteobacteria

Generate energy by respiration with sulfur-containing compounds

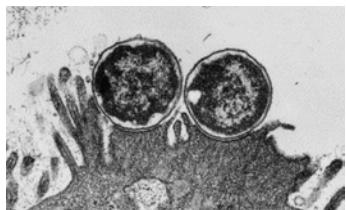


Bile acids are the source of taurine

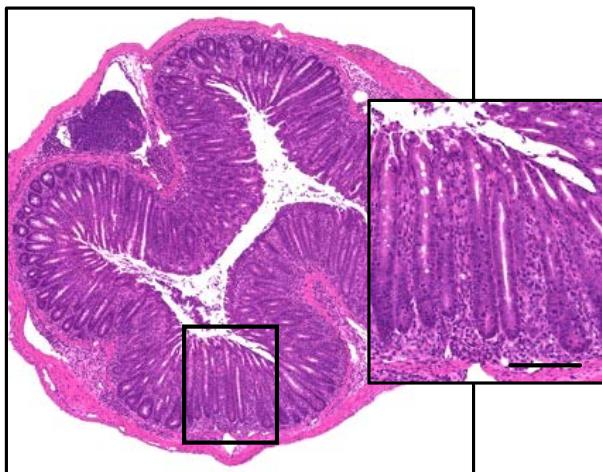


Taurine enhances resistance to infection

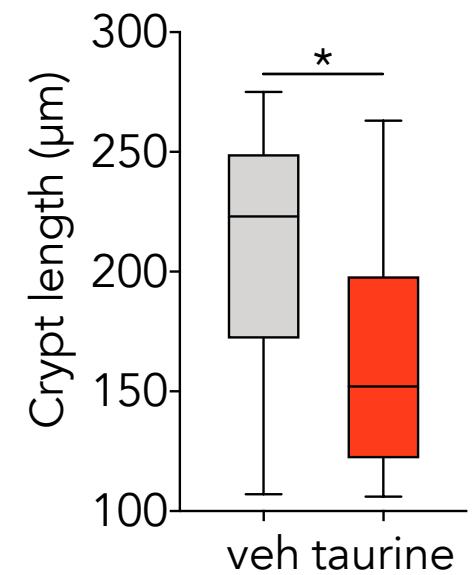
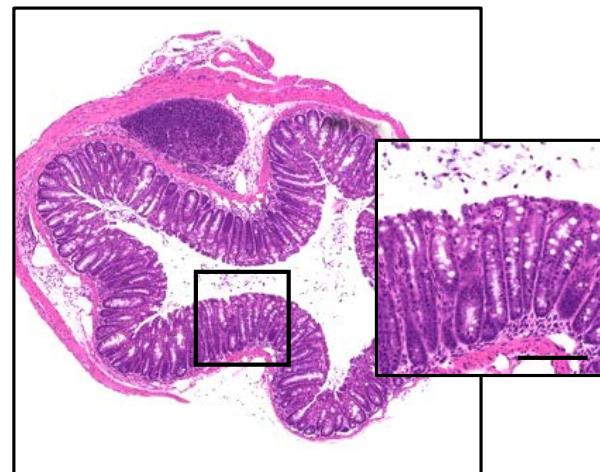
Citrobacter rodentium



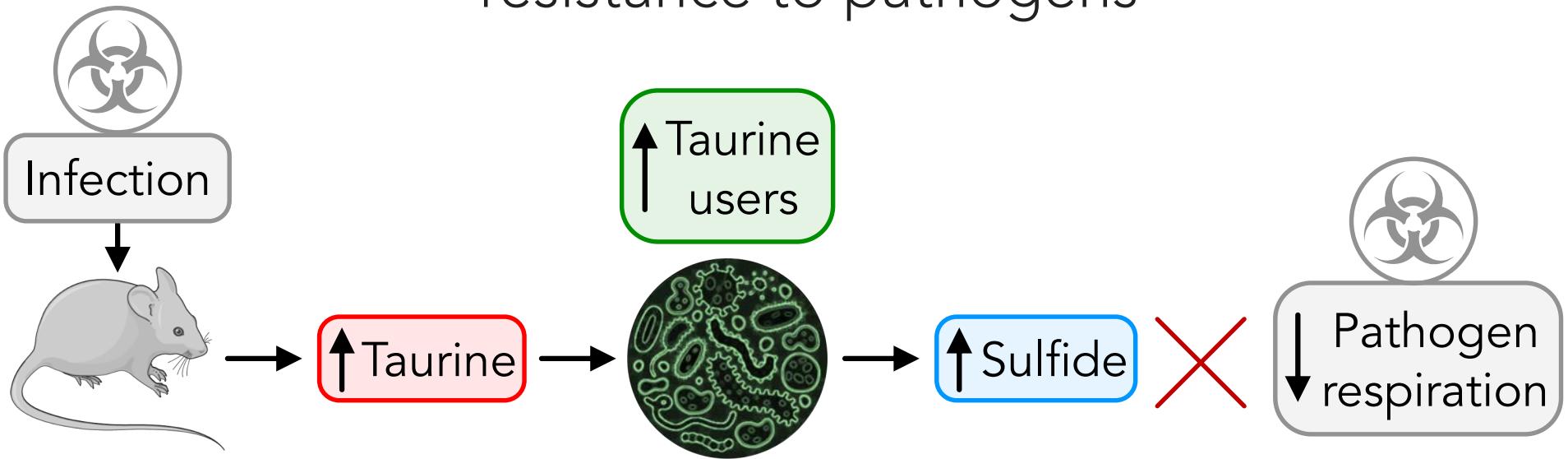
vehicle



taurine



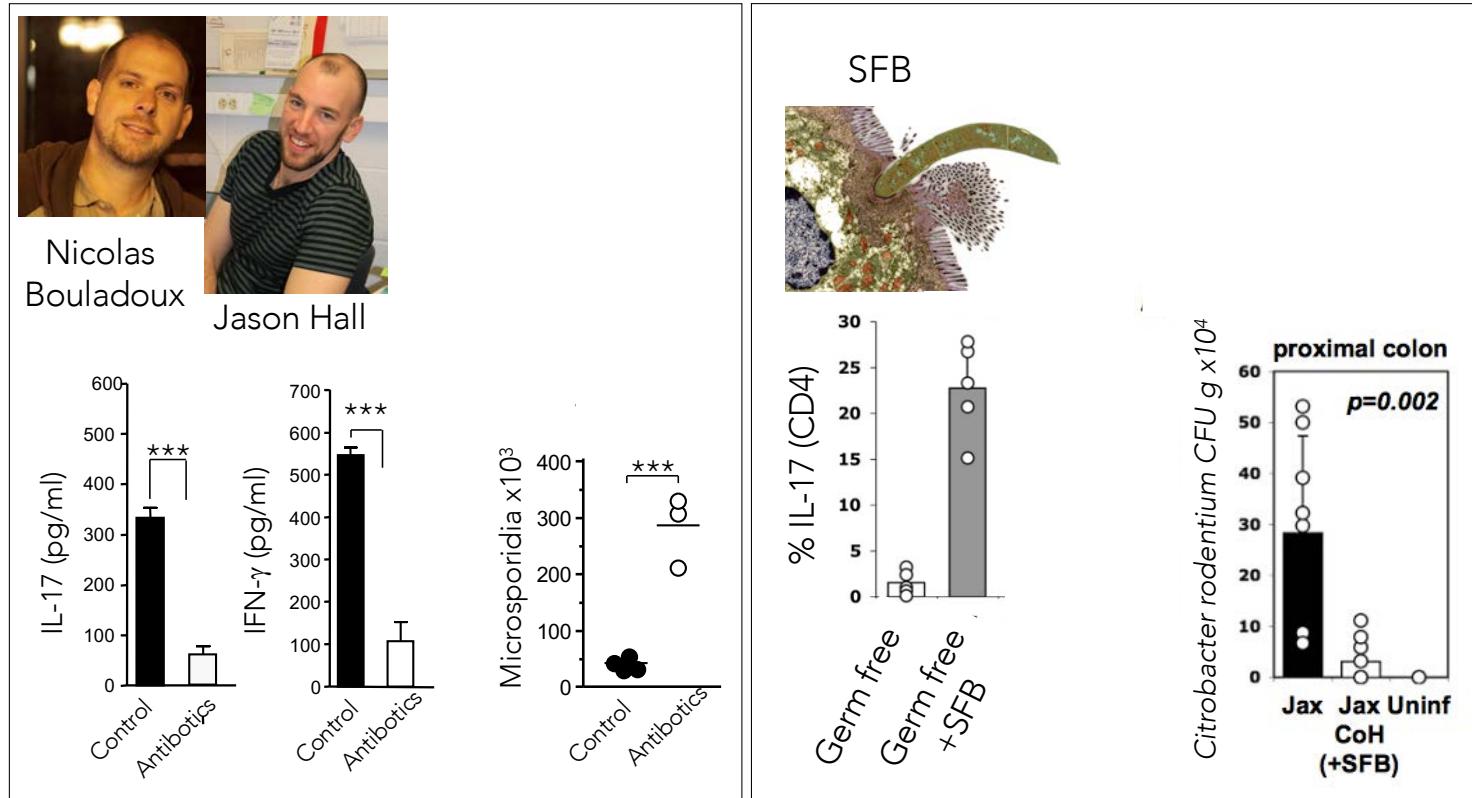
Infection trains the host for microbiota-enhanced resistance to pathogens



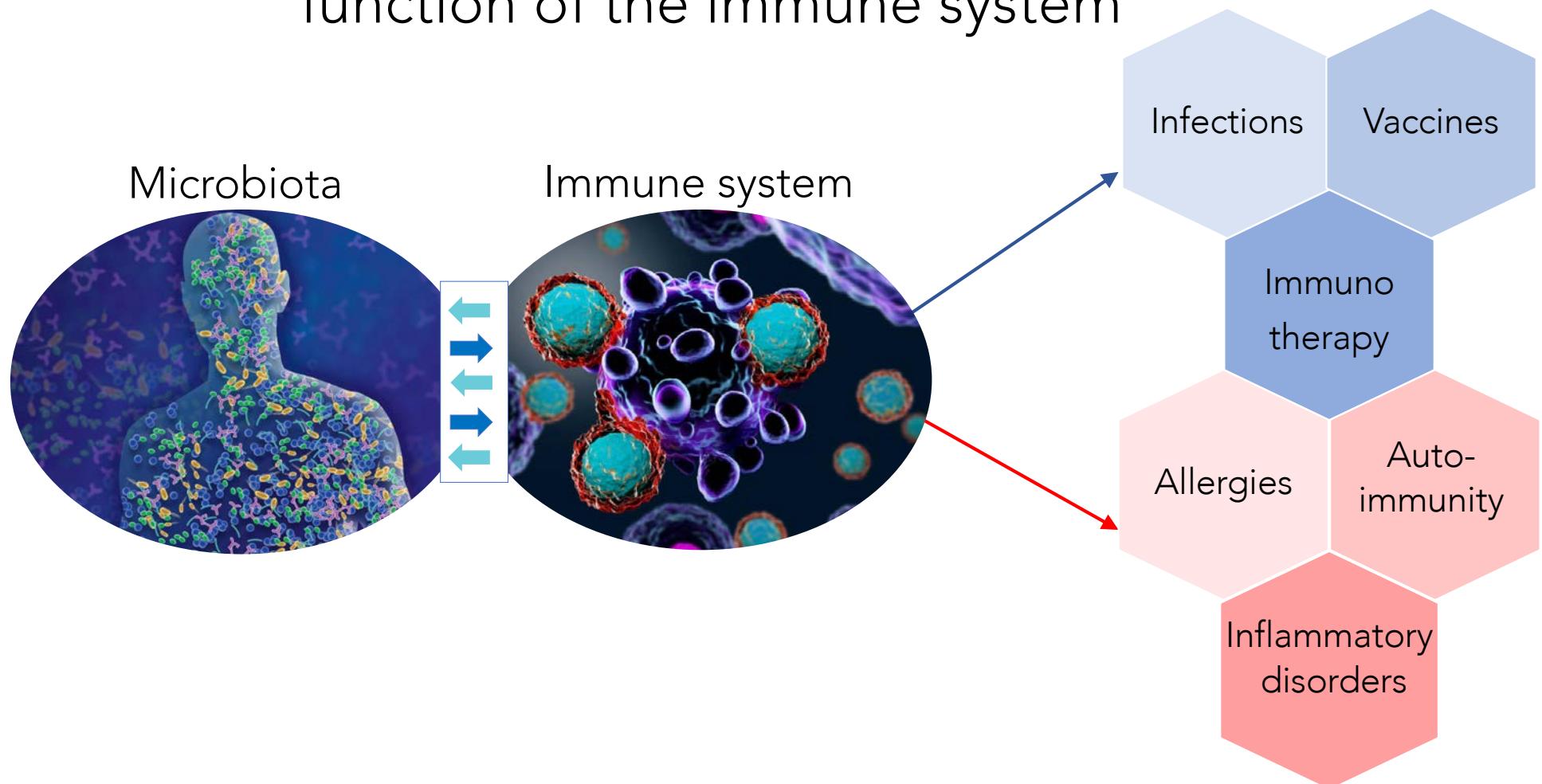
- Microbiota can be “trained,” like immune system
- Training metabolite has potential therapeutic value

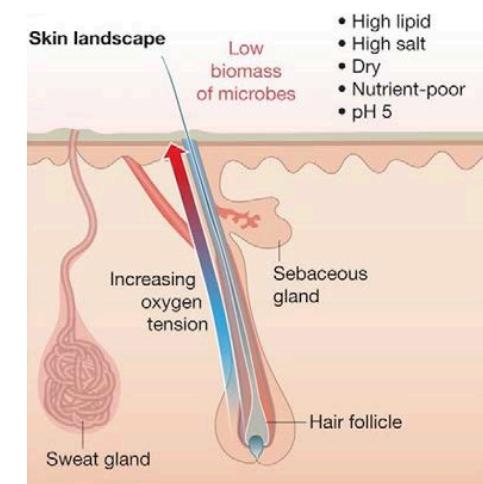
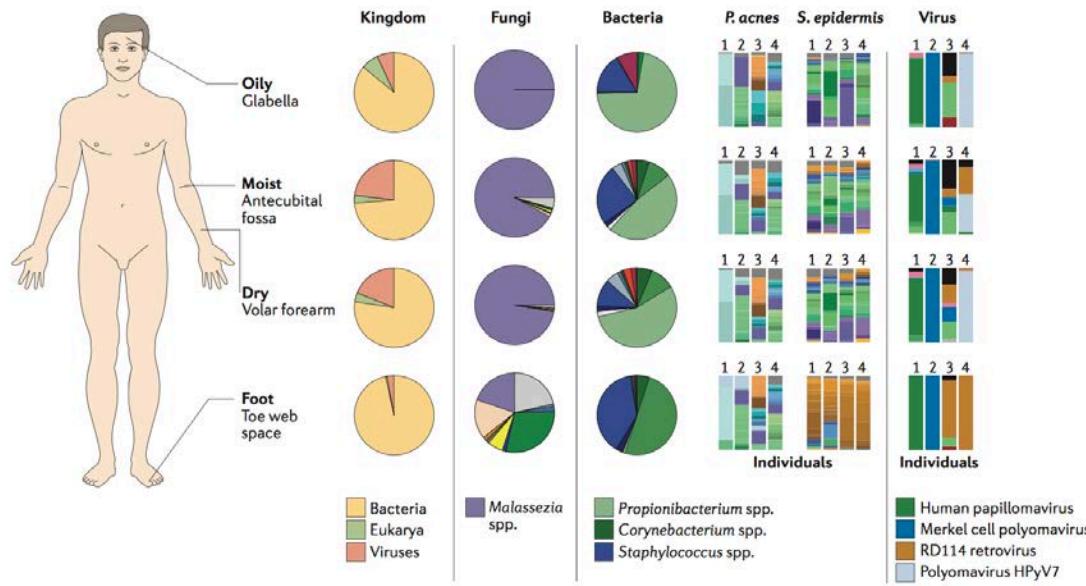
Stacy et al., *Cell* (2021)

The gut microbiota is an endogenous adjuvant for host protective immune responses



The microbiota control the development and function of the immune system





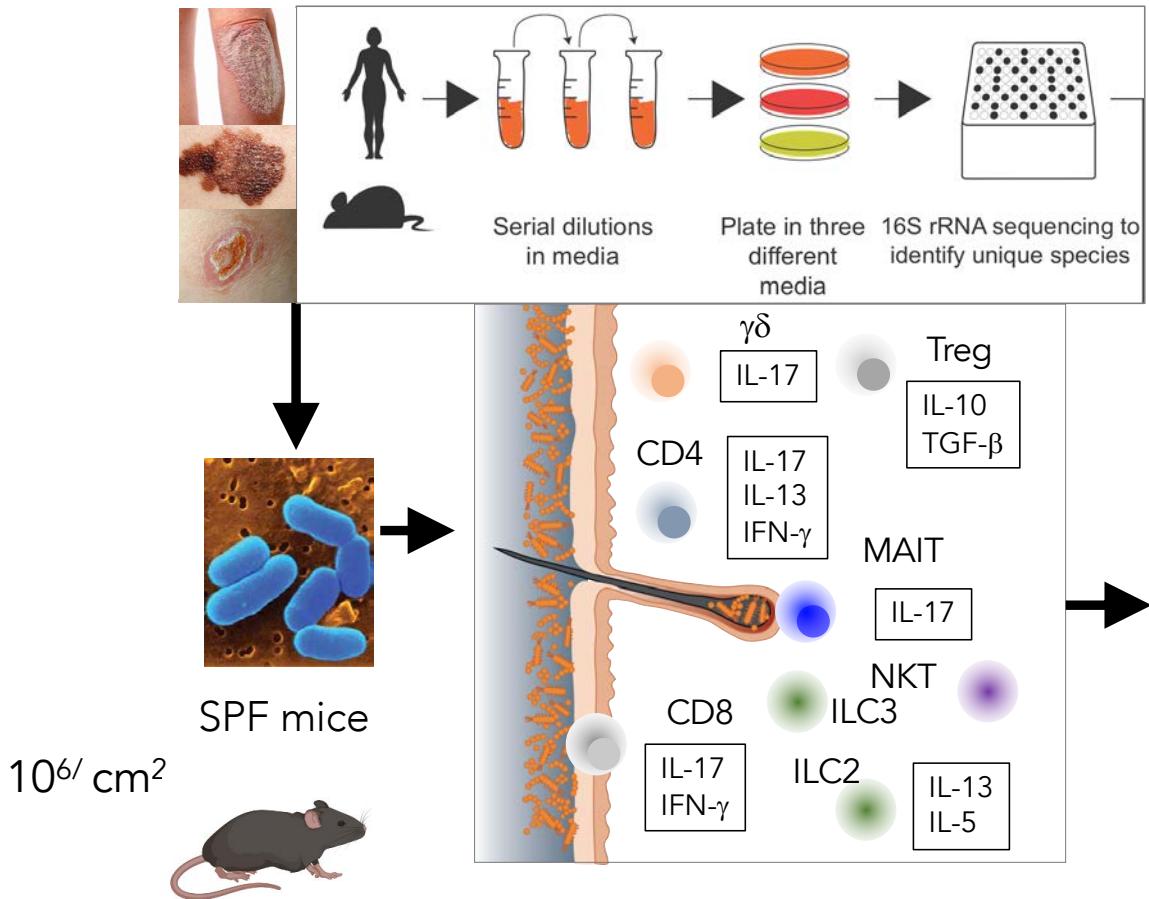
Chen, Nature 2018



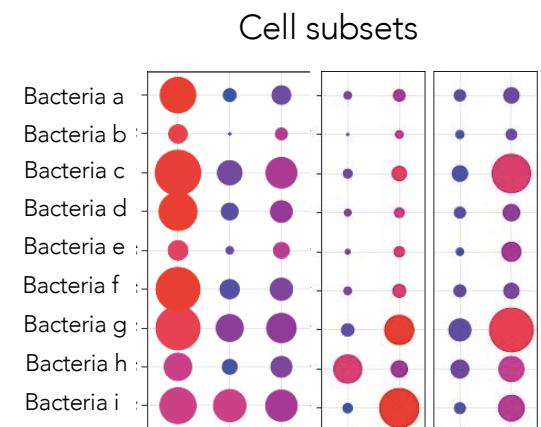
Shruti Naik
(Assistant Professor NYU)

The skin microbiota control tissue immunity

Naik, Science 2012
Naik, Nature 2015

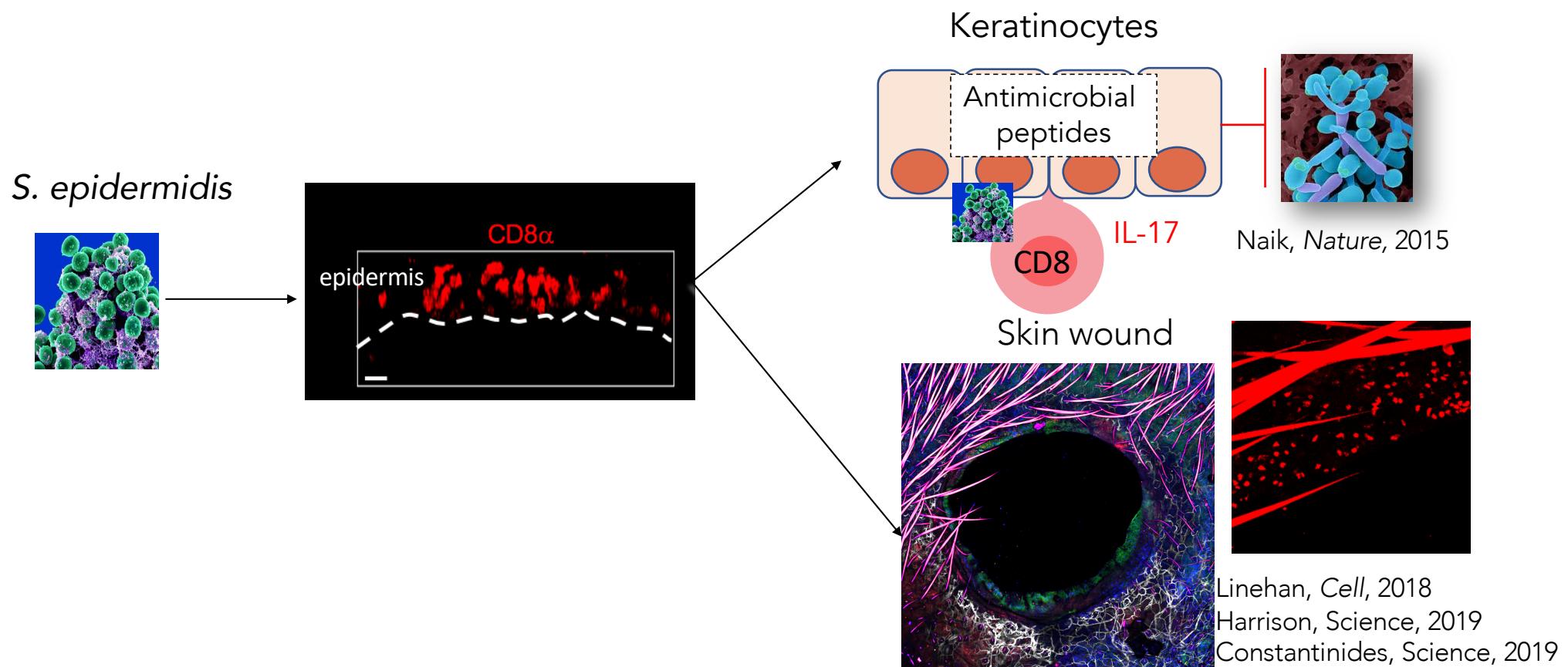


Defined microbes
impose specific immune
signature



- Naik, *Science*, 2012
- Naik, *Nature*, 2015
- Byrd, *STM*, 2017
- Ridaura, *JEM*, 2018
- Linehan, *Cell*, 2018
- Tamoutounour, *PNAS*, 2019
- Harrison, *Science*, 2019
- Constantinides, *Science*, 2019

S. epidermidis-induced CD8 T cells promote antimicrobial defense and tissue repair



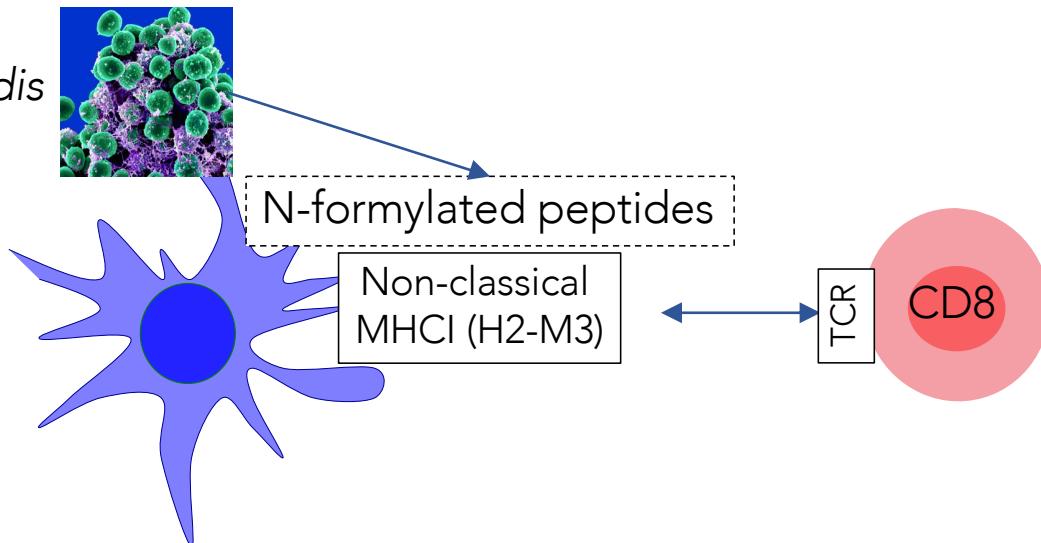
Microbiota
derived
Antigens



Self-antigens
Pathogens
Food derived antigens
Allergens

S. epidermidis specific CD8 T cells recognize N-formylated peptides antigens via non-classical MHCI

S. epidermidis



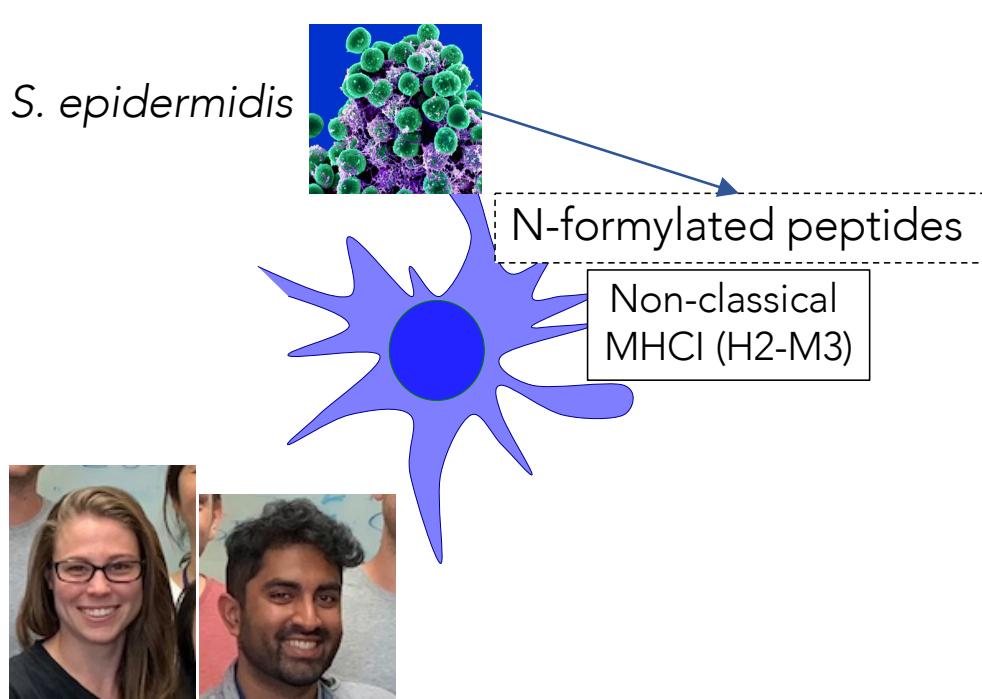
N-formyl methionine peptides: formylation required for initiation of translation in bacteria



John Linehan
(Genentech)

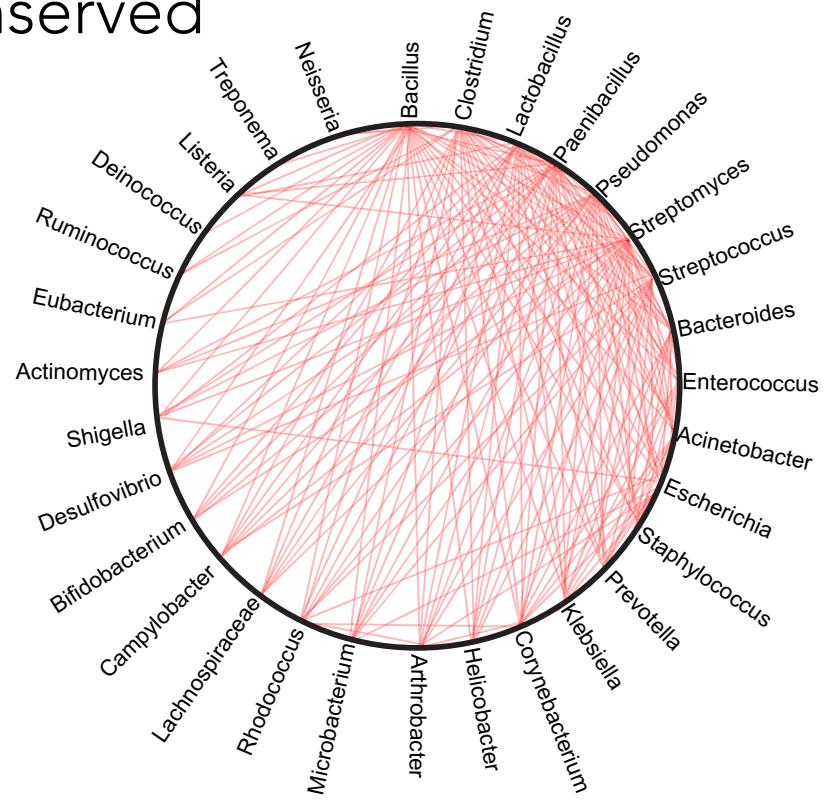
Linehan, *Cell*, 2018

Commensal derived N-formylated peptides can be highly conserved



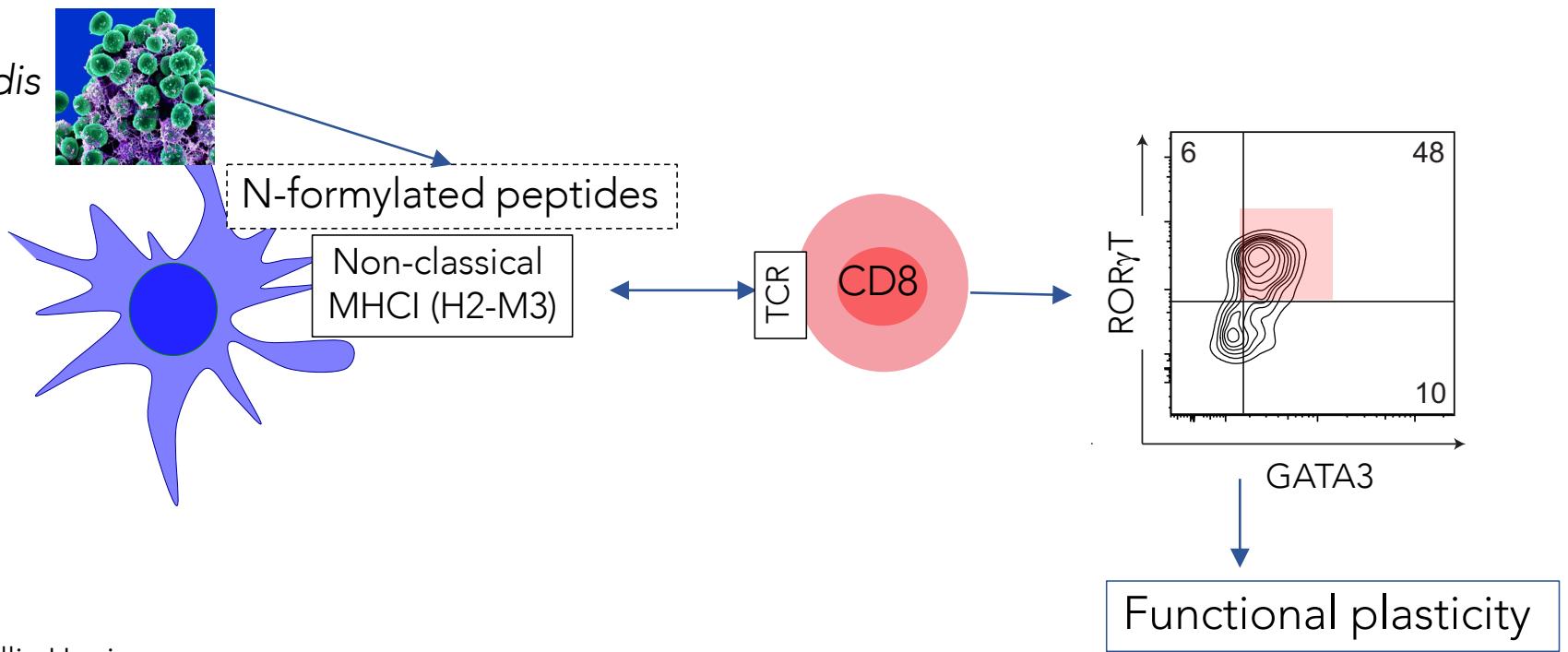
Taylor Farley Siddharth Krishnamurthy

Fiona Powrie (Oxford) & Federica Sallusto (ETH Zurich)



Commensal specific CD8 T cells express a paradoxical Type 17/Type 2 signature

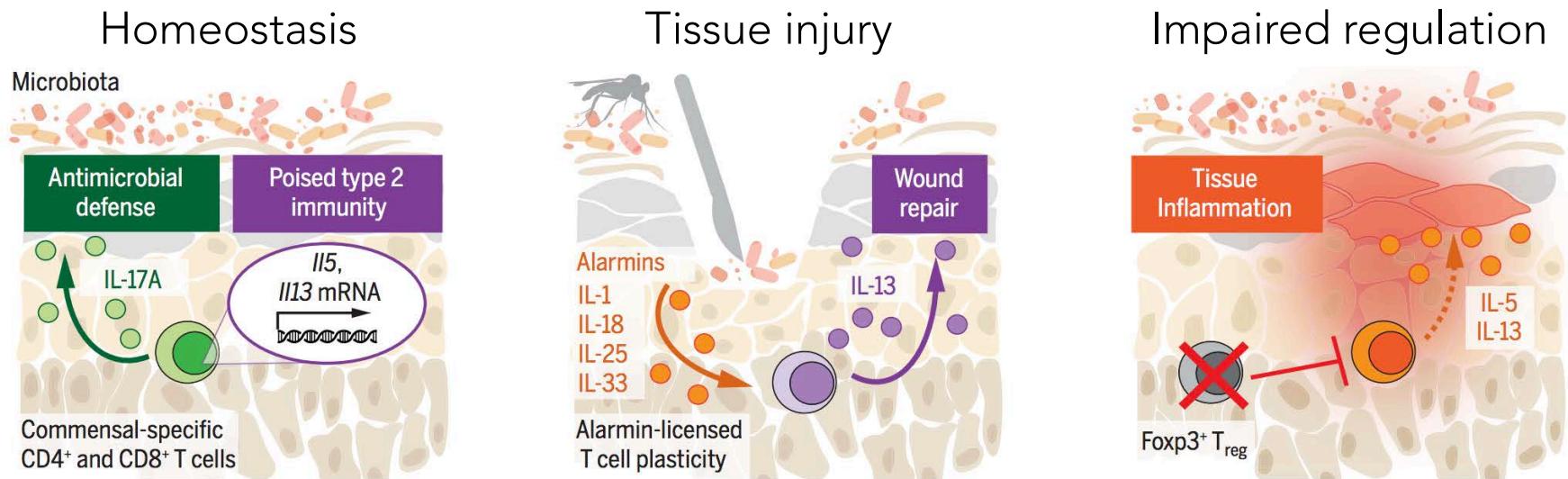
S. epidermidis



Ollie Harrison
(Assistant Professor Benaroya Institute)

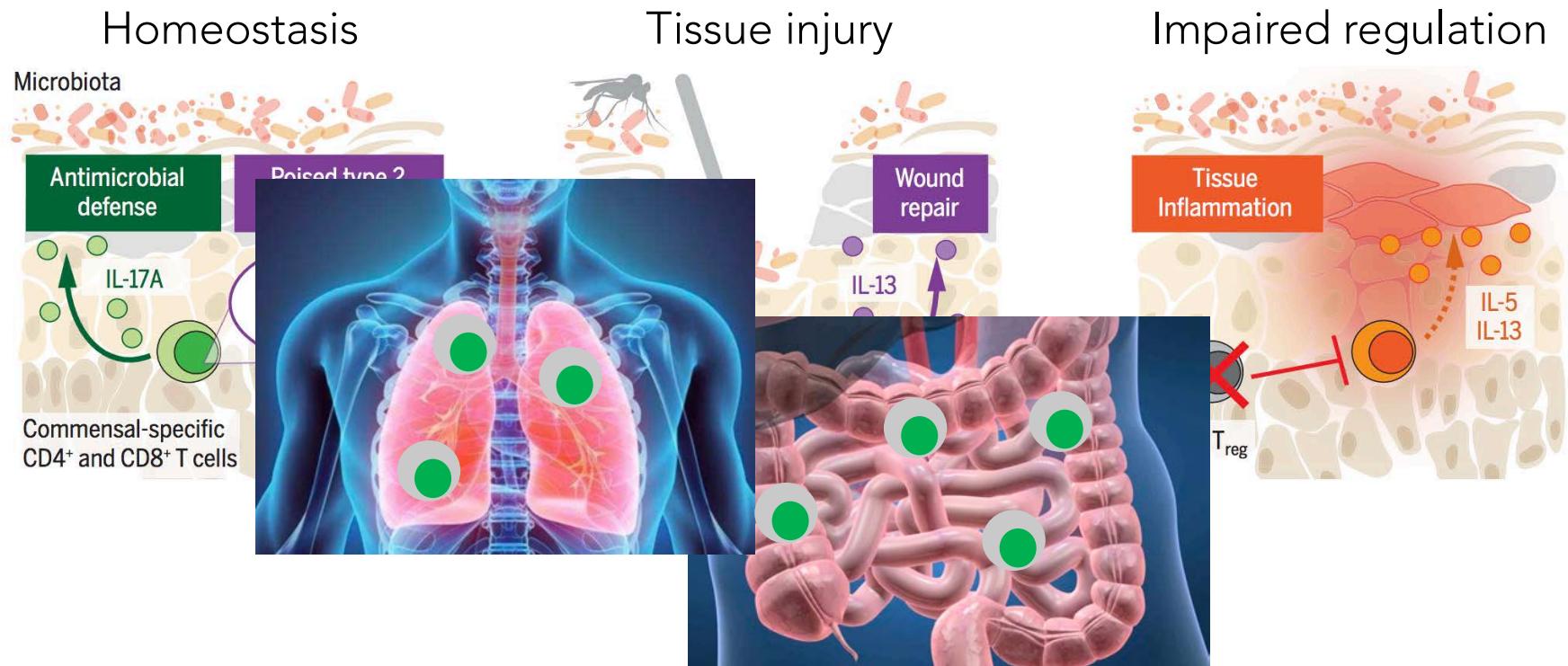
Harrison, Science, 2019

Commensal-specific T cell plasticity promotes rapid tissue adaptation to injury

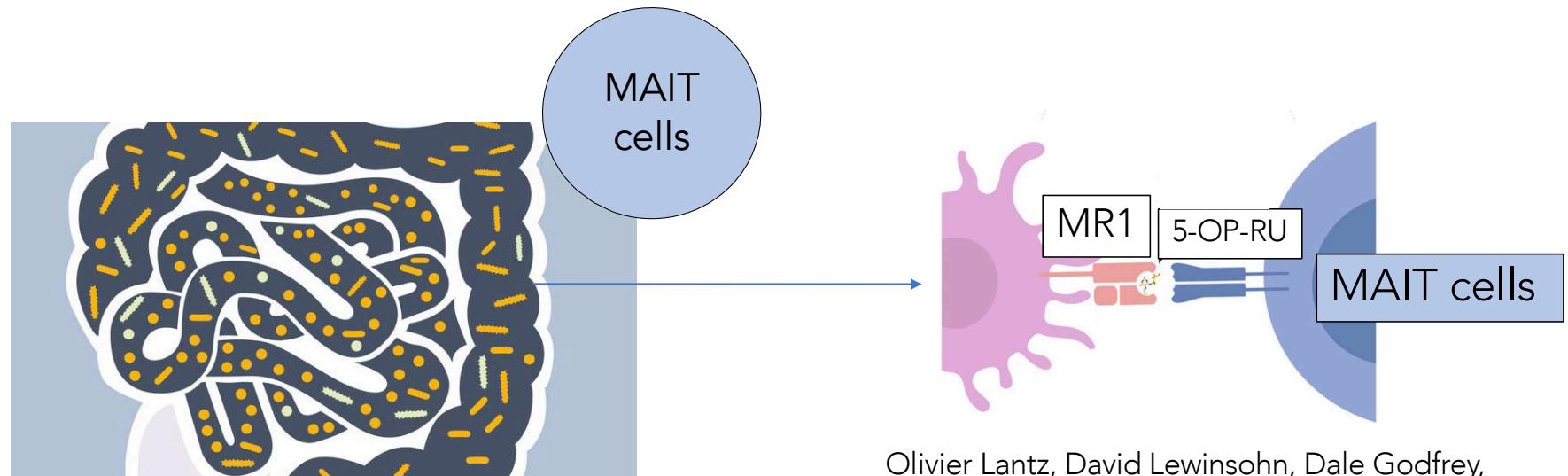


Harrison, Science, 2019

Microbiota specific Tissue resident T cells



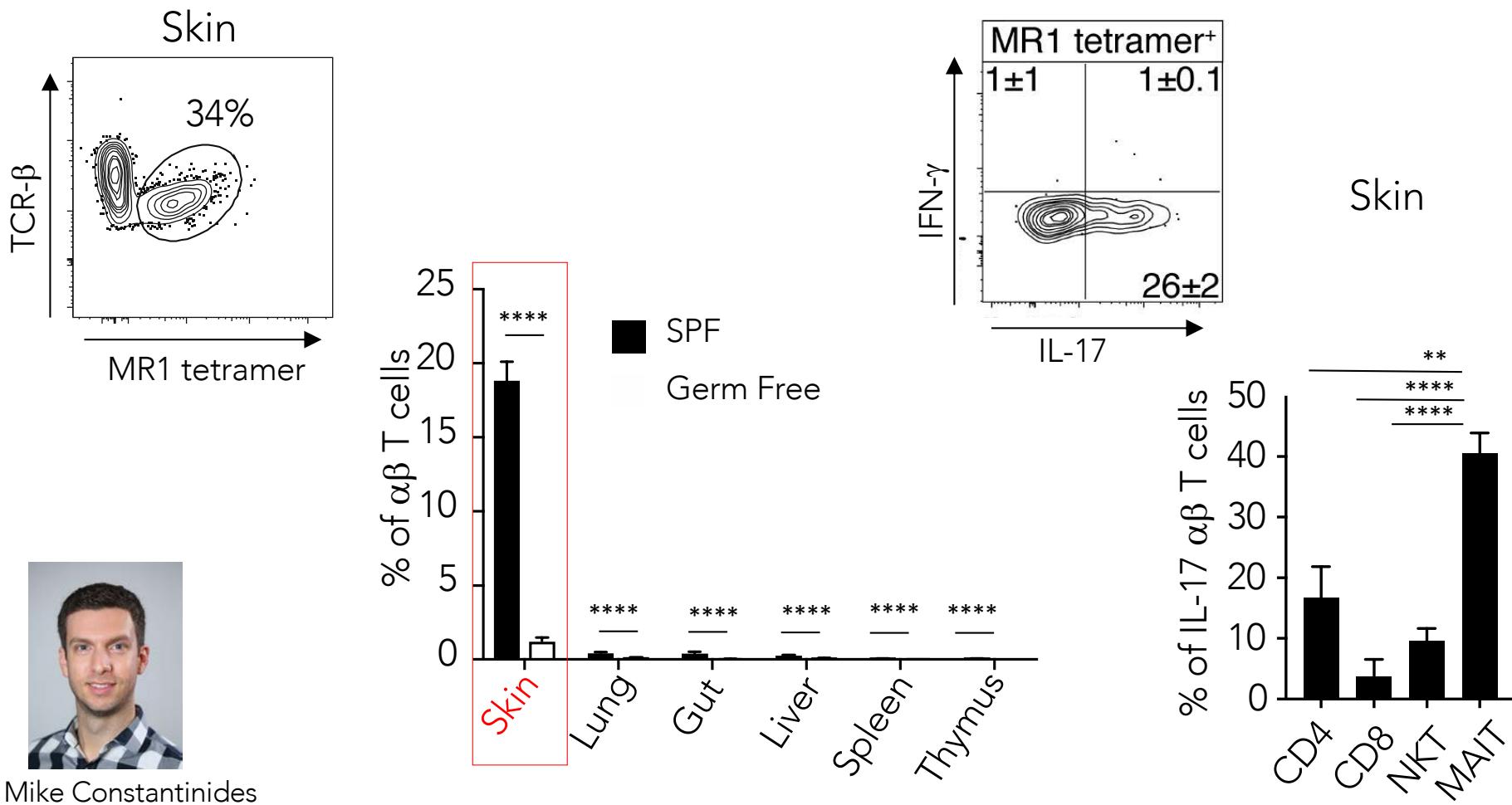
MAIT cells recognize **Antigens** derived from the microbial vitamin B2 (riboflavin) metabolic pathway



Olivier Lantz, David Lewinsohn, Dale Godfrey,
James McCluskey, Jamie Rossjohn, Paul Kleinerman...

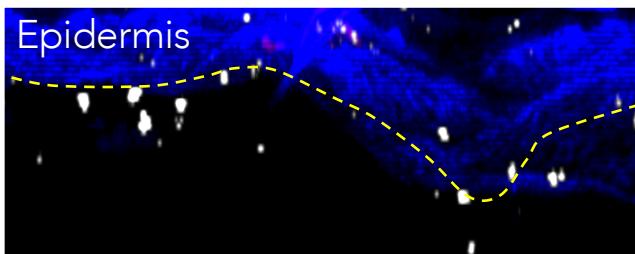
- 2-10 % of human blood and skin T cells (up to 45 % in the liver)
- Frequencies are low in mice (< 1%)....

MAIT cells are highly represented within the skin

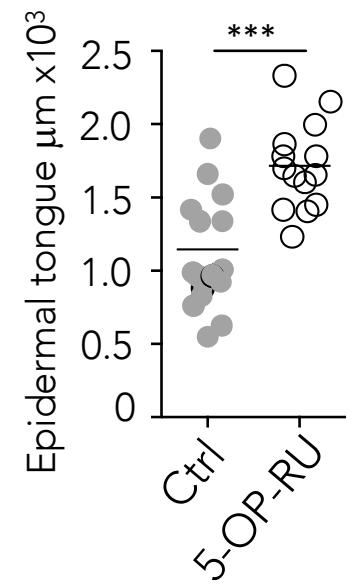
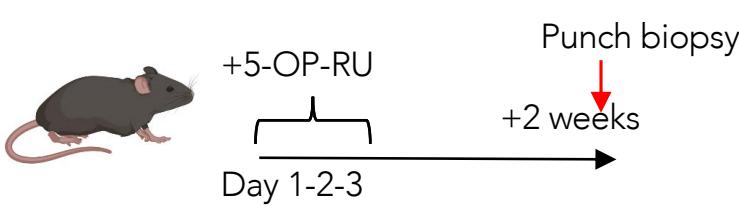
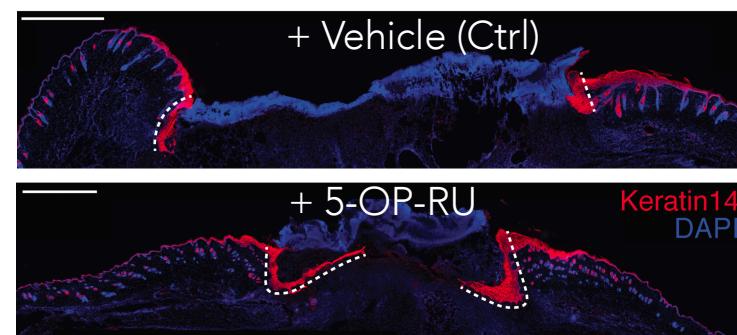
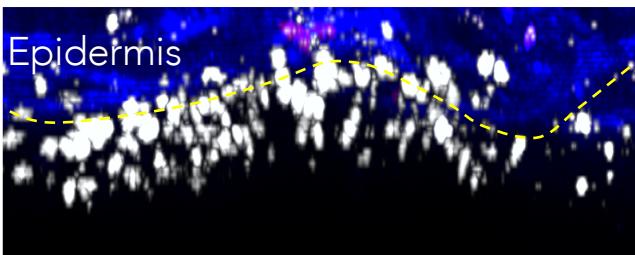


Local increase of MAIT cells promotes Tissue repair

Vehicle (Ctrl)

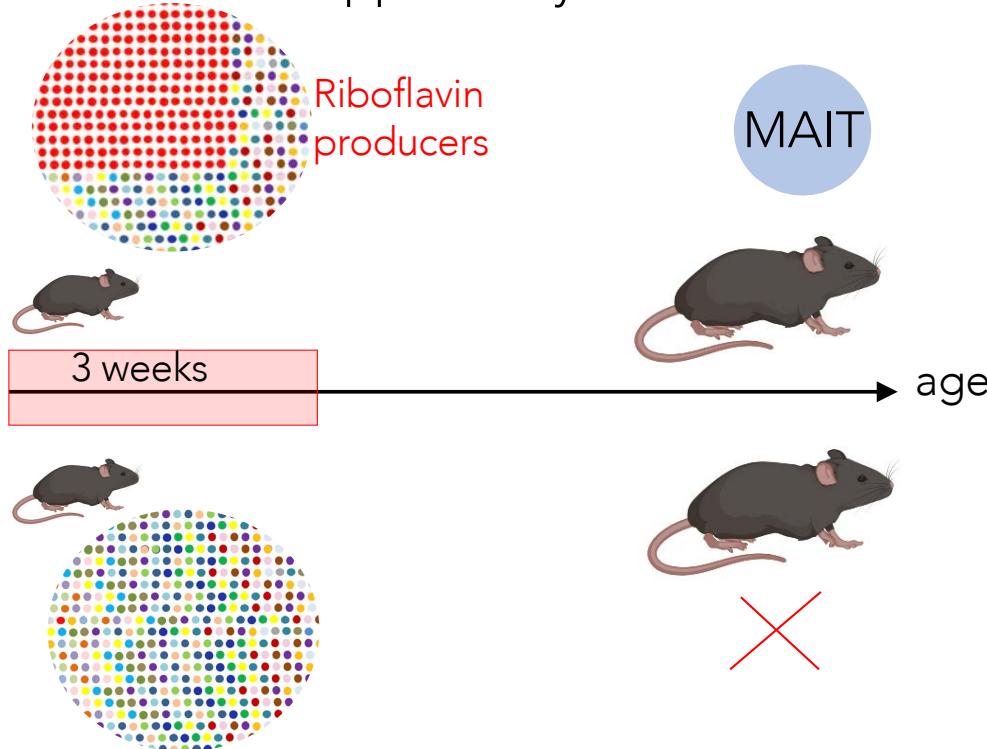


Topical 5-OP-RU



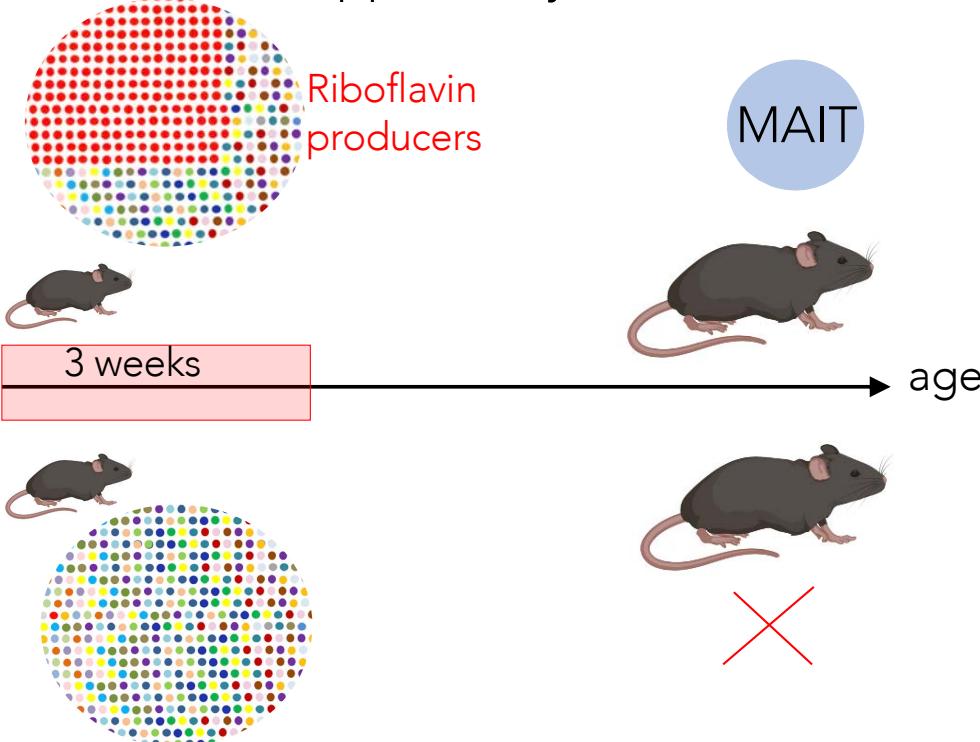
MAIT cells depend on exposure to defined microbes during a specific developmental window, after which development is permanently impaired

"Window of opportunity"

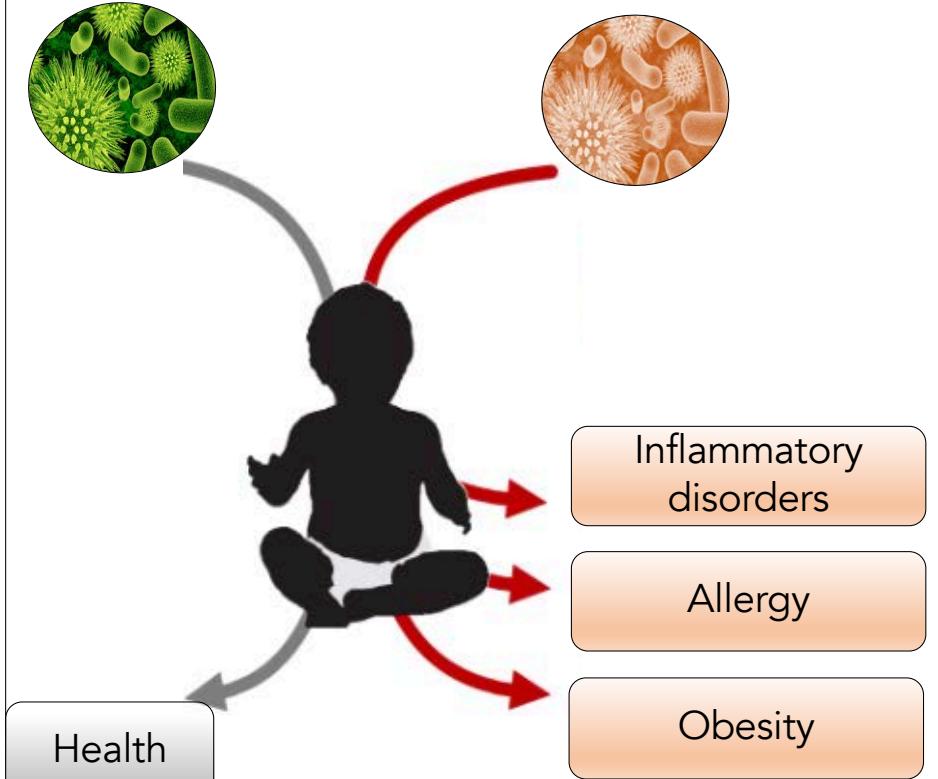


Constantinides, *Science*, 2019

"Window of opportunity"

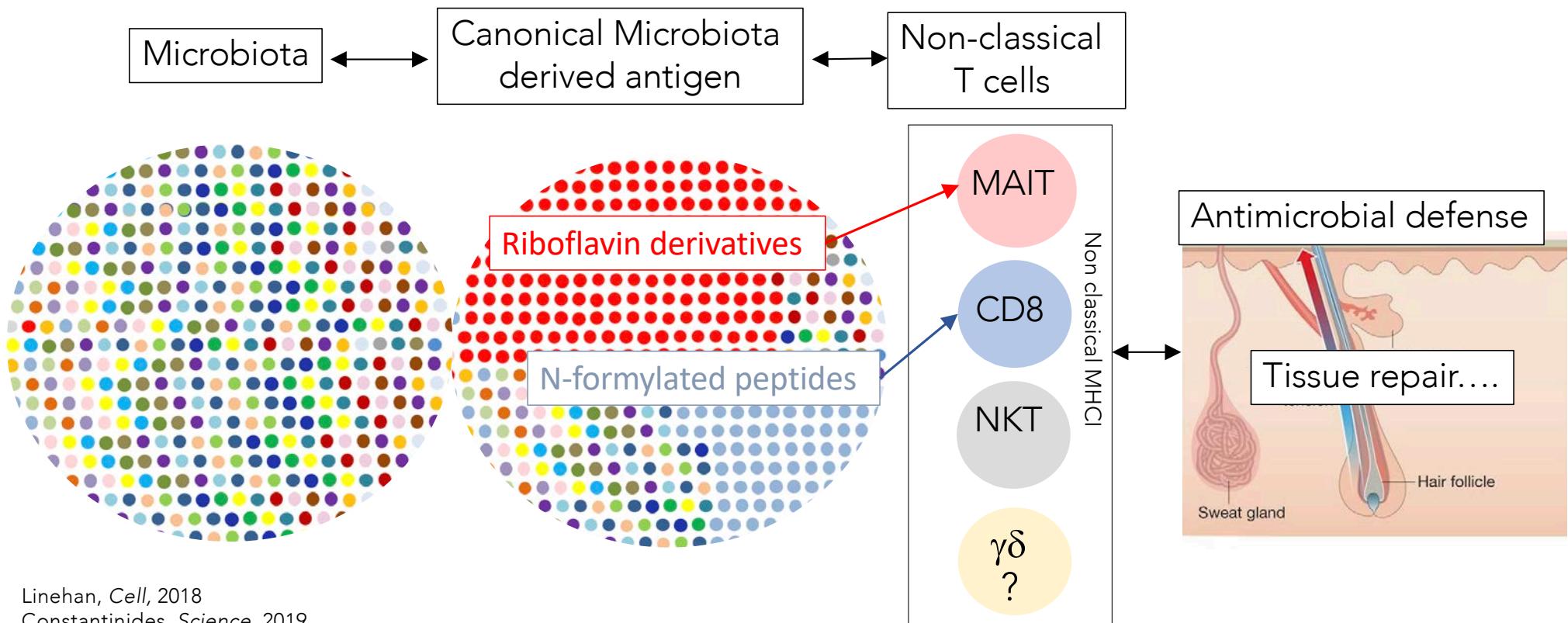


Long term impact of early life microbiota



Cell Host Microbe, 2013, Scharschmidt, Immunity, 2015, Mao,
Nature, 2018, Nabhani, Immunity, 2019, Cahenzli,, Olszak, Science,
2012, An, Cell, 2014, Nabhani Immunity 2019...

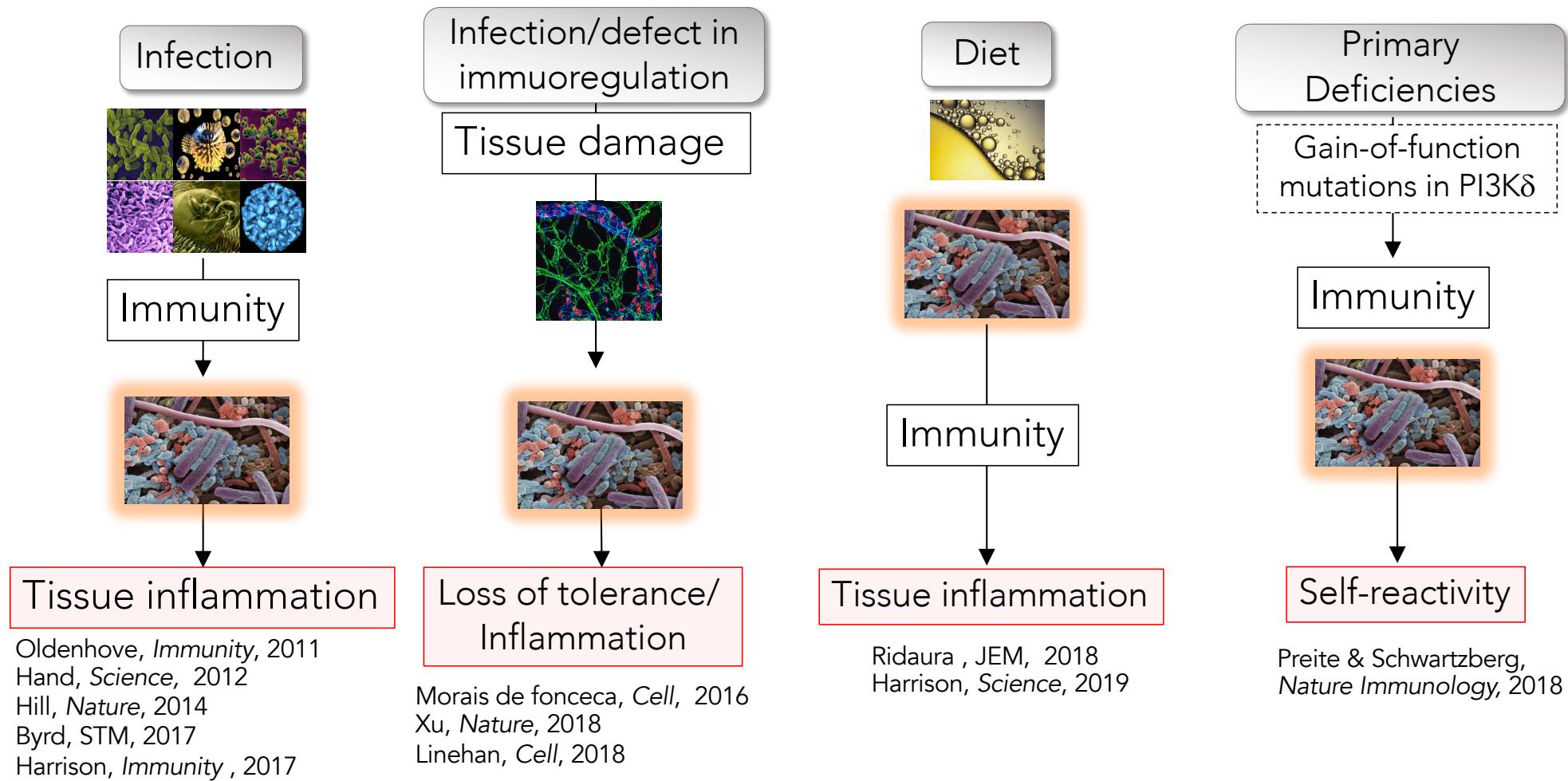
Conserved microbiota antigens/non-conventional T cell: promotion of tissue homeostasis



Linehan, Cell, 2018

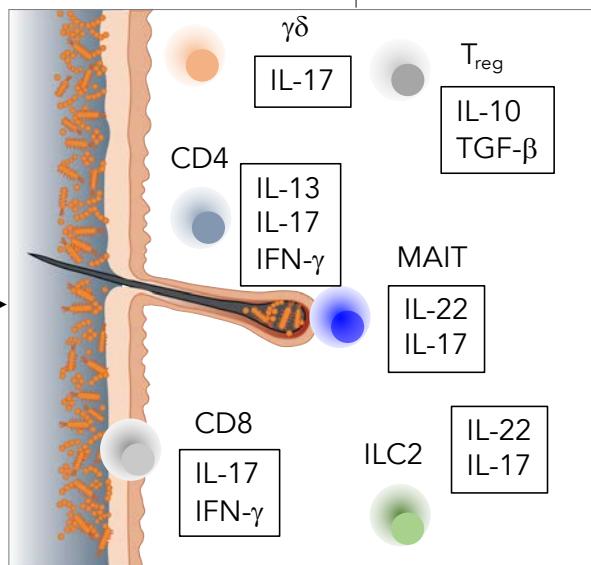
Constantinides, Science, 2019

Pathogenic immunity to the microbiota





Mining the Microbiome...



For a novel class of therapies

- Microbiota transplant
- Microbiota consortium
- Microbiota derived products/antigens
- Prebiotic



Control of Infection

Vaccine

Immunotherapy

Autoimmunity

Metabolic syndrome
Inflammatory Disorder

Allergy

As a biomarker

- Microbial communities
- Function
- Metabolites
- Immune response to the microbiota

MIS section

Nicolas Bouladoux
Seong-Ji Han Nicholas Collins
Michael Constantinides
Neris Michel Enamorado Escalona
Eduard Ansaldo Gine
Siddharth Krishnarmurthy
Pete Kulalert

Ai Ing Lim
Verena Link
Djalma Lima Junior
Apollo Stacy
Ivan Vujkovic-Cvijin
Hugh Welles
Alexandria Wells
Taylor Farley
Indira Rao
Taryn McFadden
Louis Gil Acevedo
Kimberly Webber
Ejae Louis



NIAID Microbiome Program

Xing He
Juliana Perez-Chaparro
Shreni Mistry
Andrew Burns
Tam Tran



Acknowledgements



Comparative Medicine Branch, OCICB, RTB, CHI

NIAID Collaborators: Jason Brenchley (LVD), Pamela Schwartzberg (LISB), Ronald Germain (LISB), Michael Grigg (LPD), Thomas Kristie (LVD), Joshua Milner (LID), Michail Lionakis (LCIM), Alan Sher (LPD), Tom Nutman (LPD) Irini Sereti (LIR), Daniel Barber (LPD), Robert Seder (VRC), Heather Hickman (NIAID), Jonathan Yewdell (LVD), John Mascola (VRC), Julie Ledgerwood (VRC), Mario Roederer (VRC) Graham Barney (VRC), Nancy Sullivan (VRC)....

NIH Collaborators: Avinash Bhandoola (NCI), Remy Bosselut (NCI), Mariana Kaplan (NIAMS), John O'Shea (NIAMS), Barbara Rehermann (NIDDK), Julie Segre (NHGRI), Giorgio Trinchieri (NCI), Vanja Lazarevic (NCI), Niki Moutsopoulos (NIDCR), Robert Seder (VRC), Dorian McGavern (NINDS), Nicholas Restifo (NCI), Heather Cameron (NIMH), Alexander Chesler (NCCIH)...

Extramural Collaborators: Erin Adams (U Chicago), Jeffrey Aube (UNC), Daniel Cua (Janssen), Michael Fischbach (Stanford U), Erin Chen (Stanford U), Dan Littman (NYU), Miriam Merad (Mt Sinai), Federica Sallusto (ETH, Zurich), Chyung-Ru Wang (Northwestern U), Tiffany Scharschmidt (UCSF), Gwendolyn Randolph (WashU), Boris Striepen (Upenn), Igor Brodsky (Upenn), Fiona Powrie (Oxford U), Susan Schwab (NYU), Joseph Urban (USDA), Gerard Eber (Pasteur Institute), Rob Knight (UCSD), Bana Jabri (U Chicago)...